

AMENDMENTS TO THE SPECIFICATION

Please amend the paragraph beginning on page 3, line 16, to read as follows:

Fig. 2 shows the multiple alignment of amino acid sequences of IPMDH and ICDH from various biological species (see also Table 1). The partial amino acid sequences in Fig. 2 are shown as sequence SEQ ID:1 to SEQ ID:48 in order in the sequence listing.

Please amend the paragraph beginning on page 3, line 26, to read as follows:

Fig. 6 shows the nucleotide sequence (nucleotides 1-576 of SEQ ID: 49, top strand) and amino acid sequence (amino acid residues 1-192 of SEQ ID: 50, bottom strand) of *Sulfolobus* sp. *leuB* gene.

Please amend the paragraph beginning on page 3, line 28, to read as follows:

Fig. 7 shows the nucleotide sequence (nucleotides 577-1014 of SEQ ID: 49, top strand) and amino acid sequence (amino acid residues 193-337 of SEQ ID: 50, bottom strand) of *Sulfolobus* sp. *leuB* gene (continuation of Fig. 6).

Please amend the paragraph beginning on page 4, line 4, to read as follows:

Fig. 9 shows the multiple alignment of amino acid sequences of IPMDH and ICDH. The sequences with (ICDH) represent ICDH sequence and the sequences without the indication represent the IPMDH sequence. N. Cra: *Neurospora crassa* (SEQ IDs: 57-59), S. Cer: *Saccharomyces cerevisiae* (SEQ IDs: 60-62), A. tum: *Agrobacterium tumefaciens* (SEQ IDs: 63-65), B. sub: *Bacillus subtilis* (SEQ IDs: 66-68), E. Col: *Escherichia coli* (SEQ IDs: 69-71), T. The: *Thermus thermophilus* (SEQ IDs: 72-74), Sub sp.#7: *Sulfolobus* stain #7 (SEQ IDs: 75-77), Cs. Cer: *Saccharomyces cerevisiae* (ICDH) (SEQ IDs: 78-80), CB. Tau: *Bos taurus*(ICDH) (SEQ IDs: 81-83), CB. Sub: *Bacillus subtilis*(ICDH) (SEQ IDs: 84-86), CE. Col: *Escherichia coli* (ICDH) (SEQ IDs: 87-89).

Please amend the paragraph beginning on page 4, line 17, to read as follows:

Fig. 13 shows the multiple alignment of IPMDH and ICDH. The partial amino acid sequences in Fig. 13 are shown as sequence SEQ ID:95 to SEQ ID:104 in order in the sequence listing.

Please amend the paragraph beginning on page 17, Table 1, to read as follows:

Table 1

Multiple alignment of amino acid sequences of IPMDH and ICDH

| Enzyme and species                          | Partial amino acid sequence                 |    |     |     |     |     |     |     |
|---------------------------------------------|---------------------------------------------|----|-----|-----|-----|-----|-----|-----|
| IPMDH                                       | 89                                          | 97 | 150 | 158 | 256 | 263 | 280 | 285 |
| <i>Sulfolobus</i> sp. strain □              | YDMYANIRP---IAKVG-LNFA---VHGAAFDI---MMYERM  |    |     |     |     |     |     |     |
| <u>strain 7</u>                             |                                             |    |     |     |     |     |     |     |
| <i>Thermus thermophilus</i>                 | QDLFANLRP---VARVA-FEAA---VHGSAPDI---MMLEHA  |    |     |     |     |     |     |     |
| <i>Bacillus subtilis</i>                    | LDLFANLRP---VIREG-FKMA---VHGSAPDI---MLLRTS  |    |     |     |     |     |     |     |
| <i>Escherichia coli</i>                     | FKLFNSNLRP---IARIA-FESA---AGGSAPDI---LLLRTS |    |     |     |     |     |     |     |
| <i>Agrobacterium tumefaciens</i>            | LELFANLRP---IASVA-FELA---VHGSAPDI---MCLRTS  |    |     |     |     |     |     |     |
| <i>Saccharomyces cerevisiae</i>             | LQLYANLRP---ITRMAAF-MA---CHGSAPDL---MMLKLS  |    |     |     |     |     |     |     |
| <i>Neurospora crassa</i>                    | LGTYGNLRP---IARLAGF-LA---IHGSAPDI---MMLRTS  |    |     |     |     |     |     |     |
| ICDH                                        | 89                                          | 97 | 150 | 158 | 256 | 263 | 280 | 285 |
| <i>Saccharomyces cerevisiae</i>             | FGLFANVRP---VIRYA-FEYA---VHGSAPDI---MMLNHM  |    |     |     |     |     |     |     |
| <i>Bos Taurus</i> (3/4)                     | FDLYANVRP---IAEFA-FEYA---VHGTAAPDI---MMLRHM |    |     |     |     |     |     |     |
| <i>Bacillus subtilis</i>                    | LDLFVCLRP---LVRAA-IDYA---THGTAAPKY---LLEHL  |    |     |     |     |     |     |     |
| <i>Escherichia coli</i>                     | LDLYICLRP---LVRAA-IEYA---THGTAAPKY---MMLRHM |    |     |     |     |     |     |     |
| Ancestral species<br>(predicted)            | xDLxANLRP---IARxAxFExA---VHGSAPDI---MMLxxx  |    |     |     |     |     |     |     |
| modified amino acids and<br>their positions | L                                           | L  | R   | A   | S   | P   | L   |     |
|                                             | <a region> <b region> <c region> <d region> |    |     |     |     |     |     |     |
|                                             | b' b"                                       |    |     |     |     |     |     |     |